

Exhibit 3

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ_184 1433 aa

Sequence 2: G_kaustophilus 1444 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 99

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-22024725.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:31068

Alignment Score 8866

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060823-22024725.aln]

```

SEQ_184      -----MVTKEQKERFLILLEQLKMTSDEWMPHFREAAIRKVVIDKEEKSWHFYFQ 50
G_kaustophilus MMLRGEQTDVMVTKEQKERFLILLEQLKMTSDEWMPHFREAAIRKVVIDKEEKSWHFYFQ 60
                *****

SEQ_184      FDNVLPVHVYKTFADRLQTAFRHIAAVRHTMEVEAPRVTEADVQAYWPLCLAEIQEGMSP 110
G_kaustophilus FDNVLPVHVYKTFADRLQTAFRHIAAVRHTMEVEAPRVTEADVQAYWPLCLAEIQEGMSP 120
                *****

SEQ_184      LVDWLSRQTPPELKGKLLVVARHEAEALAIKRRFAKKIADVYASFGFPPLQLDVSVEPSK 170
G_kaustophilus LVDWLSRQTPPELKGKLLVVARHEAEALAIKRRFAKKIADVYASFGFPPLQLDVSVEPSK 180
                *****

SEQ_184      QEMEQLAQKQOEDEERALAVLTDLAREEEKAASAPPSGPLVIGYPIRDEEPVRRLETIV 230
G_kaustophilus QEMEQLAQKQOEDEERALAVLTDLAREEEKAASAPPSGPLVIGYPIRDEEPVRRLETIV 240
                *****

SEQ_184      EEERRVVVQGYVFDAEVSELKSGRTLLTMKITDYTNSILVKMFSDRKEDAELMSGVKKGM 290
G_kaustophilus EEERRVVVQGYVFDAEVSELKSGRTLLTMKITDYTNSILVKMFSDRKEDAELMSGVKKGM 300
                *****

SEQ_184      WVKVRGSVQNDTFVRDLVIIANDLNEIAANERQDTAPEGEKRVELHLHTPMSQMDAVTSV 350
G_kaustophilus WVKVRGSVQNDTFVRDLVIIANDLNEIAANERQDTAPEGEKRVELHLHTPMSQMDAVTSV 360
                *****

SEQ_184      TKLIEQAKKWGHPAIAVTDHAVVQSFPEAYSAAKKHGMKVIYGLEANIVDDGVPIAYNET 410
G_kaustophilus TKLIEQAKKWGHPAIAVTDHAVVQSFPEAYSAAKKHGMKVIYGLEANIVDDGVPIAYNET 420
                *****

SEQ_184      HRRLSEETYVVFDEVTTGLSAVYNTIIELAAVKVVDGEIIDRFMSFANPGHPLSVTTMEL 470
G_kaustophilus HRRLSEETYVVFDEVTTGLSAVYNTIIELAAVKVVDGEIIDRFMSFANPGHPLSVTTMEL 480
                *****

SEQ_184      TGITDEMVKDAPKPDDEVLARFVDWAGDATLVAHNASFDIGFLNAGLARMGRGKIANPVID 530
G_kaustophilus TGITDEMVKDAPKPDDEVLARFVDWAGDATLVAHNASFDIGFLNAGLARMGRGKIANPVID 540
                *****

SEQ_184      TLELARFLYPDLKNHRLNTLCKKFDIELTQHHRAIYDAEATGHLLMRLLKEAEERGILFH 590
G_kaustophilus TLELARFLYPDLKNHRLNTLCKKFDIELTQHHRAIYDAEATGHLLMRLLKEAEERGILFH 600
                *****

```

SEQ_184	DELNSRTHSEASYRLARPFHVTLQAQNETGLKNLFKLVSLSHIQYFHRVPRIPRSVLVKH	650
G_kaustophilus	DELNSRTHSEASYRLARPFHVTLQAQNETGLKNLFKLVSLSHIQYFHRVPRIPRSVLVKH	660

SEQ_184	RDGLLVGSGCDKGELFDNLIQKAPEEVEDIARFYDFLEVHPPDVYKPLIEMDYVKDEEMI	710
G_kaustophilus	RDGLLVGSGCDKGELFDNLIQKAPEEVEDIARFYDFLEVHPPDVYKPLIEMDYVKDEEMI	720

SEQ_184	KNIIRSIVALGEKLDIPVVATGNVHYLNPEDKIYRKILIHSSQGGANPLNRHELDPDVFRT	770
G_kaustophilus	KNIIRSIVALGEKLDIPVVATGNVHYLNPEDKIYRKILIHSSQGGANPLNRHELDPDVFRT	780

SEQ_184	TNEMLDCFSFLGPEKAKEIVVDNTQKIASLIGDVKPIKDELYTPRIEGADEEIREMSYRR	830
G_kaustophilus	TNEMLDCFSFLGPEKAKEIVVDNTQKIASLIGDVKPIKDELYTPRIEGADEEIREMSYRR	840

SEQ_184	AKEIYGDPLPKLVEERLEKELKSIIGHGFAVIYLIHSHKLVKKSLLDDGYLVGSRGSGVSSSF	890
G_kaustophilus	AKEIYGDPLPKLVEERLEKELKSIIGHGFAVIYLIHSHKLVKKSLLDDGYLVGSRGSGVSSSF	900

SEQ_184	VATMTEITEVNPLPPHYVCPNCKHSEFFNDGSGVSGFDLPDKNCPRCGTYKKDGHDI PF	950
G_kaustophilus	VATMTEITEVNPLPPHYVCPNCKHSEFFNDGSGVSGFDLPDKNCPRCGTYKKDGHDI PF	960

SEQ_184	ETFLGFGKGDKVPDIDLNFSGEYQPRAHNYTKVLFGEDNVYRAGTIGTVADKTAYGFVKAY	1010
G_kaustophilus	ETFLGFGKGDKVPDIDLNFSGEYQPRAHNYTKVLFGEDNVYRAGTIGTVADKTAYGFVKAY	1020

SEQ_184	ASDHNLELRGAIEID-LAAGCTGVKRTTGQHPGGIIVVPDYMEIYDFTPIQYPADDTSSSEW	1069
G_kaustophilus	ASDHNLELRGAIEIDRLAAGCTGVKRTTGQHPGGIIVVPDYMEIYDFTPIQYPADDTSSSEW	1080

SEQ_184	RTTHFDHFSIHDLNLLKLDILGHDDPTVIRMLQDLSGIDPKTIPTDDPDVMGIFSSTEPLG	1129
G_kaustophilus	RTTHFDHFSIHDLNLLKLDILGHDDPTVIRMLQDLSGIDPKTIPTDDPDVMGIFSSTEPLG	1140

SEQ_184	VTPEQIMCNVGTIGIPEFGTRFVRQMLEETRPKTFSELVQISGLSHGTDVWLGN AQELIQ	1189
G_kaustophilus	VTPEQIMCNVGTIGIPEFGTRFVRQMLEETRPKTFSELVQISGLSHGTDVWLGN AQELIQ	1200

SEQ_184	NGTCTLSEVIGCRDDIMVYLIYRGLEPSLAFKIMESVRKKGKGLTPEFEAEMRKHDVPEWY	1249
G_kaustophilus	NGTCTLSEVIGCRDDIMVYLIYRGLEPSLAFKIMESVRKKGKGLTPEFEAEMRKHDVPEWY	1260

SEQ_184	IDSCKKIKYMFPAHAAAYVLMVAVRIAYFKVHHPLLYYASYFTVRAEDFDLDAMIKGSPA	1309
G_kaustophilus	IDSCKKIKYMFPAHAAAYVLMVAVRIAYFKVHHPLLYYASYFTVRAEDFDLDAMIKGSAA	1320

SEQ_184	IRKRIEEINAKGIQATAKEKSLTTLVLEVALEMCERGFSFKNIDLYRSQATEFVIDGNSLI	1369
G_kaustophilus	IRKRIEEINAKGIQATAKEKSLTTLVLEVALEMCERGFSFKNIDLYRSQATEFVIDGNSLI	1380

SEQ_184	PPFNAIPGLGTNVAQAIVRAREEGEFLSKEDLQQRGKLSKTLLEYLESRGCLDSLDPHNQ	1429
G_kaustophilus	PPFNAIPGLGTNVAQAIVRAREEGEFLSKEDLQQRGKLSKTLLEYLESRGCLDSLDPHNQ	1440

SEQ_184	LSLF	1433
G_kaustophilus	LSLF	1444
